Title: >US-09-415-540-2 Title: \text{VS-09-415-540-2} Perfect Score: 1274 N.A. Sequence: 1 CANGAGGTTNGGGGGTTTTTTTTTTTTTTTTTTTTTTTTT	MPsrch_nn n.a n.a. database search, using Smith-Waterman algorithm kun on: Mon Dec 27 11:37:08 1999; MasPar time 2173.47 Seconds 1374.544 Million cell updates/sec	**************************************	[
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Title Desci Perfe Searched: Nmatch Scoring table: Comp: STD : TABLE default Dbase 0; Query 0 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: Database: embl-est58 1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2
6:em_est9 7:em_gss1

8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13 13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17 17:gb_est11 18:gb_est15 15:gb_est16 16:gb_est27 17:gb_est18 18:gb_est19 19:gb_est2 20:gb_est20 19:gb_est20 19:gb_est5 19:gb_est5 19:gb_est6 19:gb_est5 19:gb_est6 19:

Statistics: Mean 11.461; Variance 2.065; scale, 5.550

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID .	Description	Pred: No.
o	1 710	55.7	751	22	AI078153	oz30c03.x1 Soares_tota	
a	2 626	49.1		17	AA694204	zi42cl2.sl Soares_feta	
a	3 596	46.8	704	28	AI565600	to16f09.x1 NCI_CGAP_U	t 0.00e+00
n	571	44.8		18	AA766473	oa35g06.sl NCI_CGAP_GC	٠,
a	5 567	44.5	_	24	AI215898	qm35h09.x1 NCI_CGAP_L	
a	5 541	42.5		14	AA493425	ne48h03.sl NCI_CGAP_C	
۵	7 529	41.5	_	20	AA932061	oo59b07.sl NCI_CGAP_L	
Ω	529	41.5		36	AA075389	zm87c06.s1 Stratagene	
O	9 523	41.1		24	AI219448	qh13c03.x1 Soares_NFL_	
C 1	520	40.8	_	18	AA777776	zi95h10.sl Soares_feta	

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	. 1.3.1					
source	1127 1110 1100 1100 1100 1100 1100 1100	TITLE JOURNAL COMMENT	REFERENCE	KEYWORDS SOURCE ORGANISM	ACCESSION NID VERSION	RESULT 1 LOCUS DEFINITION
1. 751; 1. 751; 1. 751; 1. 751; 1. 751; 1. 751; 2. 752; 2. 7530; 2. 7530; 2. 7530; 2. 7530; 2. 7530; 3	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2041 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 452.	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) On Jan 19, 1998 this sequence version replaced gi:2282347.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 751) NCI-CGAP.http://www.ncbi.nlm.nih.gov/ncicgap.	EST. human. Homo sapiens	PYROPHOSPHATASE;, mRNA sequence. AI078153 93412561 AI078153.1 GI:3412561	A1078153 751 bp mRNA EST 01-OCT-1998 oz30c03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676836 3',similar to SW:IPYR_BOVIN P37980 INORGANIC

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BASE COUNT
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                                                                                                           670 GTTTGACATCATTGATATCATAATAATTGGCTGCATCAGGATCATCCACATTAAAGGCAA 729
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                        730 TGACTTTTCCATCGGTTTCCCC
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  TGACTTTCCAGTCGGTTTCCCC
                                                                     GTTTGACATCATTGATATCATTATAATTGGCTGCATCAGGATCATCCACATTAATGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructed by Bento Soares /db_xref="taxon:9606"
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98.5%;
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536
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0; Mismatches 9
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JOURNAL
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122 AAAAGTTATCTTAGTTGAGATATGAAAAATGCTTTAGATGGATAACATTCTGAGTATATT
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                                                                                       TGCACATCTATTCACAAGTGACTTCCAAATGACAACTGCTTTGATATTTAAGCATGTGCT 121
                                                                                                                                               CAGCAAAATAATTTTATTTCCTAACATATGGTAACATATACATCCAATATGTGCTCCCCT
                                                            TGCACATCTATTCACAAGTGACTTCCAAATGACAACTGCTTTGATATTTAAGCATGTGCT
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Unpublished (1997)
On Nov 12, 1997 this sequence version replaced gi:2559131.
                                                                                                                                                                                                                                                                  h 49.1%;
Similarity 99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA694204 639 bp mRNA EST 16-DEC-1997 z142c12:s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:433462 3' similar to SW:IPYR_BOVIN P37980 INORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Allen, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pharmacia), digested with Pac I and cloned into and Eco RI sites of the modified pT7T3 vector. I
                                                                                                                                                                                                                                                                                                                                         /dev_stage="20 week-post conception fetus"
/lab_host≐"DH10B (ampicillin resistant)"
126.c 107 g 214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    constructed by Bento Soares and M.Fatima Bonaldo
/db_xref="GDB:1333231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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Pred. No. 0.00e+00
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                                                                                                                Seq F
                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome. Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                 Tissue Procurement: Chri. Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                              Robert_Strausberg@nih.gov
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.85 kb. Life Technologies catalog #
                                                          /organism="Homo sapiens"
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. NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2179241 3'
SW:IPYR_BOVIN P37980 INORGANIC PYROPHOSPHATASE;, mrna
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                       sequence.
AA766473
g2817711
AA766473.1
                                                                           AA7,66473 646 bp mrna EST 28-JAN-1998 oa35g06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307002 similar to SW:IPYR_BOVIN P37980 INORGANIC PYROPHOSPHATASE;, mF
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/lab_host="DH10B"
/lab_host="DH10B"
137 c 120 g 238 t 4 other
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High quality sequence stop: 190.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GCAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
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polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="germinal center B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert_Strausberg@nih.gov
Procurement: Christopher Moskaluk, M.D.,
                               to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was
                                                                                                                                    /note-"Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; ist strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.ncbi.nlm.nih.gov/ncicgap
constructed by Bento Soares and M. Fatima
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/note="Organ: lung; Vect
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similar to
Contact: Robert Strausberg, Tel: (301) 496-1550
                                       Unpublished (1997)
On Apr 14, 1993 th
                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 564)
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/tissue_type="carcinoid"
/lab_host="DH10B"
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Homo sapiens cDNA clone IMAGE:900629 3'
N P37980 INORGANIC PYROPHOSPHATASE;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.D., Ph.D
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/clone="IMAGE:900629"
/clone_lib="NCI_CGAP_CO3"
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/lab_host="DH10B"
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Pred. No. 0.00e+00;
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oo59b07.s1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S<sub>D</sub>
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                         164
                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12,
                                                                                                                                                                                                                                                                                                                                                                                                           to Eco RI adaptors (Pharmacia), digeste cloned into the Not I and Eco RI sites pT713 vector. Library is normalized to constructed by Bento Soares and M. Fati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung; Vector: pT7T3D-Pac () modified polylinker; 1st strand cDNA was
                                                                                                                                                                                                                                                                                                       /tissue_type="carcinoid"
/lab_host="DH10B"
103 c 94 g 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www
                                                                                                                                                                                                                                                                                                                                                                                             constructed by Bento /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroendocrine lung carcinoid,
                                                                                                                                                                                                                                                                                                                                                         clone_lib="NCI_CGAP_Lu5"
                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1570453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo, sapiens"
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titute, Cancer Genome Anat
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                                                                                                                                                                                                                               Score 529; DB 20;
Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Rolman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project Unpublished (1995)

On Apr 14, 1993 this sequence version replaced gi:716386.
                                                                                                                                                                      High quality sequence stop:
                                                                                                                                                                                                                                                                                  WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should
                                                                                                                                                                                                                                                                                                                                                                                                 Tel:
                                                                                                                                                                                              Seq primer: -40Ml3 fwd. from Amersham
                                                                                                                                                                                                             This clone is available royalty-free through LLNL ; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                           Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                Washington University Sch
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zm87c06.s1 Stratagene ovarian car
clone IMAGE:544906 3' similar to
PYROPHOSPHATASE;, mRNA sequence.
                                                                                                                                                                                                                                                                            kept in mind should you use this
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
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                                      Papillary serous carcinoma, old caucasian amount
Vector; ~5' adaptor sequence: adaptor sequence: 5' CTCGAGTT
                                                                                xhoI;
                                                                       /note="Vector: Bluescript SK-; XhoI; Cloned unidirectionally.
                                                                                                                organism="Homo sapiens"
                                                                                                                                                         location/Qualifiers
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                  Average insert size: 0.8 kb; Uni-ZAP. aptor sequence: 5' GAATTCGGCACGAG 3'
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l Similarity 96.6%;
576; Conservative
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 572)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                           AI219448 572 bp mRNA EST qh13c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA IMAGE:1844548 3' similar to SW:IPYR_BOVIN P37980
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                 g3801651
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                                                                                                                Homo sapiens
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/map="942A12; 11; 11q24.3-11q25"
/clone="IMAGE:544906"
/clone=Lib="Stratagene ovarian cancer (#937219)"
/sex="female"
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135 c 114 g 195 t 4 others
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                                        795 TTCGTTTTCTTAGTCACTAATGCTTTCCAATGGTCATGAGTGCTTTTAATAATATCAATG
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538 GCAAAGTCCTTTATCTTTAATTCTGCATAAAACGC
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Email: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available IMAGE Consortium (info@i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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llarity 97.68;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-*Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries; (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1844548"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by 1
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/note="Organ: pooled; Ve
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                         61 TGCACATCTATTCACAAGTGACTTCCAAATGACAACTGCTTTGATATTTAAGCATGTGCT 120
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                                                                                                                                                                     ch 40.8%;
l Similarity 99.1%;
525; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Allen, M., Bowles, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA777776 530 bp
zi95h10.s1 Soares_fetal_
clone IMAGE:448579 3' s:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYROPHOSPHATASE ;,
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                                                                                                                                                                                                                                                                              160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           est@watson.wustl.edu
                                                                                                                                                                                                                                                    /sex="male" 20 week-post conception fetus" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" 103 c 95 g 172 t
                                                                                                                                                                                                                                                                                                                                                                                                                                     constructed by Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Pharmacia), digested with Pac I and cloned into and Eco RI sites of the modified pT7T3 vector. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver spleen lNFLS library. 1st s
with a Pac I - oligo(dT) primer [5′
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
with a modified polylinker; Site_1 Pac I; Soares fetal
                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:448579"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was ligated to Eco RI adaptors
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                                                                                                                                                                 Score 520; DB 18;
Pred. No. 0.00e+00;
0; Mismatches 5;
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al_liver_spleen_1NFLS_S1
similar to SW:IPYR_BOVIN
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                                                                                                                                                                                                                                                                                Email: PC'
Th'
                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 452.
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qb91e02.x1 Soares_fetal_heart_NbHH19W Homo sapiens

IMAGE:1707482 3' similar to SW:IFYR_BOVIN P37980 IN

PYROPHOSPHATASE :, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On Sep 12, 1996 th
                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
                                        M.Fatima Bonaldo. same fetus as the
   (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the
                                                                                                                                                                                                                                                                                                            Robert Strausberg, Ph.D.
1) 496-1550
                                                                                                                                                                           /organism="Hómo sapiens"
                                                                                                                                                                                                            Location/Qualifiers
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            Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.G., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bhillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Small, K.V., Sprigs, T.A., Utterback, T.R., Welley, R., Small, R.V., Sprigs, T.A., Utterback, T.R., Welley, R., Small, R.V., Sprigs, T.A., Utterback, T.R., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA314881 528 bp mRNA EST186922 HCC cell line (matastasis to sapiens cDNA 5' end similar to similar
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyrophosphatase, mRNA sequence.
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/lab_host="DH10B (ampicillin
99 c 93 g 173 t
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/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:1967451
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                                                                                                                                                                                                                                                                                                                                                       Catarrhini;
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Cepeda, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                            GCAAGGTATGTGCAAGAGGTGAAATAATTGGCGTGAAAGTTCTAGGCATATTGGCTATGA
                                                                                                                                                                                                                         TAGTTGAAGTACCACGCTGGTCTAATGCAAAAATGGAGATTGCTACAAAGGACCCTTTAA
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                                                                                                                   ATAAAGGATATATCTGGAACTATGGTGCCATCCCTCAGACTTGGGAAGACCCAGGGCACA
                                                                                                                                                                                                                                                                                    AATATATATCTCCATTTCATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGG
                                                                                                                                                                                                                                                                                                   AATATATATCTCCATTTCATGATATTCCAATTTATGCAGATAAGGATGTGTTTCACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTGGCTCTGTGGCAGCGGCGGCAGGACTCCGGCACTATGAGCGGCTTCAGCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  information related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: Mi3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Similarity
| 526; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li.H., Meissner, P.S., Olsen, H. Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression pattern: based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTs:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="ATCC (inhost):113250"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/map="844006; 5: 5q31.1-5q31.3"
/clone_lib="HCC cell line (matas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="colon"
/ceil_type="KM12SM"
/ceil_line="KM12C(HCC)metastasis
101 c 140 g 132 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 518; DB 11;
Pred. No. 0.00e+00;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On Sep 19, 1997 this sequence version replaced
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High quality sequence st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the through contact the thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thaising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
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On Sep 12, 1996 this sequence ver
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clone IMAGE:447614 3' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier, L., Allen, M., Bowles, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Primates; 1 (bases 1 to 521)
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                                                                                                                                                                                                                                                                                                                                                                            primer: -40ml3 fwd. ET from Amersham
h quality sequence stop: 399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            est@watson.wustl.edu
                        This is a subtracted version of the original Soares
                                                                                                                                                                                    with a modified polylinker;
double-stranded cDNA was
                                                                                                                                                                                                                            /note="Organ:
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                            organism="Homo sapiens"
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                                                                                                                                                                                Spleen; Vector: pT7T3D (Pharmacia) ker; Site_1: Pac I; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dubuque, T., Geisel, G.,
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                                                                        1st strand cDNA was er [5'
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N P37980 INORGANIC
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Wilson, R.
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Query Match
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    1 (bases 1 to 580)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                           AAO75438 580 bp mRNA EST zm87c05.rl Stratagene ovarian cancer (#937219) clone IMAGE:544906 5' similar to SW:IPYR_BOVIN PYROPHOSPHÄTASE ; mRNA sequence.
                                                                                                                                       EST
                                                                            Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominid
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/lab_host="DH10B (ampicillin resistant)"
100 c 96 g 169 t
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t through one round of normalization. Library
structed by Bento Soares and M.Fatima Bonaldo."
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Pred. No. 0.00e+00;
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P. and
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                                                 C-GAATGGAAAAGGAATCAGTTGCATGAATACAACTTTGTCTGAGAGCCCCCTTCAAGTGT
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557; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WARNING: There is evidence that suggests that the 384-well plate of this clone contains both human and mouse derived Thus, the origin of this clone is uncertain. This caution kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             old caucasian. Average insert size: 0.8 kb; Uni-ZAP Vector; -5; adaptor sequence: 5; GAATTCGGCACGAG 3; adaptor sequence: 5; CTCGAGTTTTTTTTTTTTTTTT 3;"/db_xref="GDB:3923094"
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Papillary serous carcinoma, isolated
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/lab_host="SOLR (kanamycin resistant)"
107 c 141 g 149 t 2 oth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions.

The true left end of clone C47E12 is at 1 in this sequence. The true left end of clone F44D12 is at 37752 in this sequence. The true right end of clone T13H10 is at 4978 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans cosmid C47E12, complete sequence. 268882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bin/display?db=wormacesclass=Sequence sobject=C47E12
Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predictions from Genefinder available information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaughan,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sproat,J. and Wohldman,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M., Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-JAN-1996) Louis, MO 63110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The end of this sequence (37752).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone C47E12.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overlapping sections once,
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Rhabditina; Rhabditoidea; Rhal
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(bases 1 to 37855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a graphical representation of this sequence and its analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 (6466), 32-38 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z68298
                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="IV"
                                                                             /gene="C47E12.11"
|oin(959...1428,1483.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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/gene="C47E12.11"
                                                                                                                                                                                                                       'clone="C47E12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           It may be shorter because we only sequence once, or longer because we arrange for a small
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is NOT
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78 like.
                                                                             .1578,1623. .1728,1787. .2112,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .37855) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        computer analysis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1998
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EMVRDEEFYQGMIQCAKLRALARVHAENGSVIAERCEHLLSSGITGPEGHTQSRPEEL
EABATERACTMASQANCPLYVHYMSKCAAAAIAHHRKKGAVVPGEPIAGLATDCSH
YYNEDMLHAARYVMSPPLSRDPSTPSALMKLLAAGELHLTATDNCTFDCOOKSLGKDD
YYNEDMLHAARYVMSPPLSRDPSTPSALMKLLAAGELHLTATDNCTFDCOOKSLGKDD
FTKIPNCYNGYEDRMSVVMDKGYHAGIIDPMRFVAVTSTMAAKIINCYPOKGRIAVGS
DADIYIMANATRTISKDTHHHAIDFNIFEGMQVHGVPEITISRGRTVMANGQLKTVQ
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AETYDPNYQTLAGLNNDLVFGEQPGAGPRAPPPGSNPGMVGTADPNYQTLAGLNNDLV
FGGGGGGPAPPKAPTVGGKAATNDPNYQTLADLHNEEIFKEKGAKPPENVAKAATNDP
GSGQF1PLAPDSQ1VFSAVDNRKKAMEPVK1DR1PYEPSALQTPDANAN1VVKAPVRA
                                                                                                                                                                                                 /db_xref="Swiss-prot:018677"
/translation="MSLLIKNGTIVNDDAIFKSDVLVLDGRIVEIAPSIOPTPGLEVV
DATDRLVIPGGIDPHTHMQLPFMGEIAKDDFHRGTEAAVAGGTTMIIDFVIPTKGESL
LVAXDRWRGWADPKVVCDYGLSMAITSWGPEIAKEMELVTGAEYGINSFKFFLLYYAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted using Genefinder; Similarity to Mouse
Ulip protein (PIR Acc. No. S55525)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYQTLAGLRNDEIFKPKNPAAPVQPPARDVQTPFINNNDLRPKQPVQKNVKAGMYDPN
YQTLAGLNQDIFGADKKKNY"
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4669. .4767,4819. .5046)
/gene="C47E12.10"
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LAKRGMDSNDLASSTSSKHSTKKTNTSDSYSDDMSPVFLTRVSSDTRFPGATSPATCE
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                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA93104.1"
/db_xref="PID:e1344628"
/db_xref="PID:93875109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="C47E12.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEEVIESDFFLKTQLHNENELIKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAIDQNWAPVMAIPFCAPVGKRDPVLMNPIEKVKENVEIFVNYRDALKTYSDKVLEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="G1:3875108"
/db_xref="SPTREMBL:Q18676"
/translation="MANICLESIFLVLLSFFKNVVCEDQLTYEFNEQNNLEDSRKTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA93109.1
/db_xref="PID:e1344633"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(5765. .5839,5951.
/gene="C47E12.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA93102.1
/db_xref="PID:e1344626"
/db_xref="PID:g3875107"
/db_xref="GI:3875107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )LRDSDSCSEDESWDKQKSKKDVKKKKGTRGM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:3875114"
/db_xref="SPTREMBL:Q18682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA93103.1"
/db_xref="PID:e1344627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="C47E12.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MVTLSVILTKSLLLVGILFEPPYIYIIIIQLSTFLFIQCGSKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="SPTREMBL:Q18675"
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                                                                                                                                                                                                                                                                                                                                                       db_xref="GI:3875109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin(9248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="C47E12.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGLFEYSEIEKIRELFWEVEMRSSQTLVGFKNFQKCFFRKIAENYSSEVAQKFEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="PID:g3875108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48. .9333,9383. .9563,9608. .9779,9828. .10084,
.10363,11090. .11402,11451. .11771)
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gene

gene CDS:

nt(join(11905. .12121,12209. 13153,13202. .13328))

.12722,12773.

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Note: remainder of
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                       27195 CCAGGATAAACCTTTTCGACGTCATCAATGTCAATTCAACTTGTCAGCATTCTCATCGTTG 27254
                                          27315
                                                                                                                                            27255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                                                            570
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                                                                                                                                                                                                                                                                                                                      Local
AGAACTTTTACTTGCAGAACAGCTCCCCGTCCGGCAACCTTTGATCCAACATTCAATAACA 27374
                                                                          ACATTAATGGCAATGACTTTCCAGTCGGTTTCCCCCTTCGTCAATCATAGCCAATATGCCT 511
                                                                                                       ACATCAATTGCGACCAATTTCCAATCGGTCTCTCCTTCGTCAATGAGAGCCAATGTTCCG 27314
                                                                                                                                                                         CCAGGTTTCAGCCGTTTGACATCATTGATATCATTATAATTGGCTGCATCAGGATCATCC
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                           annotations omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(20994.
22791. .23873,23921. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(20994. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRVFILESPQFRLNTVARLHFDYKLQGDANLFICNDSGTKELESCFKVEGREGNDYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="molftryresgwteskalrhsadlncdfthpekcewknmadekomdskofylfekidyteffylrvgfgpskioodgdkmifygdkkreeohalfysspinconstgnltfymvynsarvevilleddckggykmifddpseekpyvdcgtiolntechaelfprdkpfrigiraygisnidgsfymidnilysaslckvgidygdffksysletgas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLASDTKVYIISRLSESGKSGSLEISKIVFTDTSDQSIC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSSKTFRPTADMPDPNVCRLLSCDFHLGHACLYESSQVSNSAMHGVANRKLNAFLTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKHIDTAAELKCDNFDTKCRWRSGGDAMVMWRRSSSILPSPLLMNATGSTVGPRGGYA
VLYVEQGTOKKSLDILRSDPITCQSLTENEFTERFWEFGQIELEACAVDLMLKDIECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="C47E12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIPRGSSPANVKLTFRKATKNFMIIIRVSSLNPDFDNMVIVDDISYRATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="cDNA EST yk220g1.3 comes from this gene; cDNA EST yk20g1.5 comes from this gene; cDNA EST yk355a12.3 comes from this gene; cDNA EST yk355a12.5 comes from this gene; cDNA EST yk358h5.3 comes from this gene; cDNA EST yk358h5.5 comes from this gene; cDNA EST yk358h5.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="C47E12
                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="predicted using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="SPTREMBL:Q18681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="PID:g3875113"
/db_xref="GI:3875113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA93108.1"
/db_xref="PID:e1344632"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          joln(17223. 17554,17603. 17779,17826. 17920,18165. 1
18384. 18571,18614. 18755,18805. 19233,19324. 19656,
20045. 20161,20208. 20324,20414. 20512)
/gene="c47E12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )OKSDLITAVEEGEEMDQGGIEFSYKEIGALLFEVGKQEHLNAKRRKKIYDLYKKFDK
SSRGQDPLHFETFYPKERLIRHDYEEAEKKAIVLANSFKQERKSSRKVKSQIKKRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDVDLASVEVVFAQKLACGEPATRQRALRVLHDWIRDQSAKKHF
DDADLMRLCKGLHYVMWMQDKMILQEELADRIGGLINIFTSEEEKVRRVACFLKSLSK
EWPHIDRWRMDKFLMEVRRMVRACETHLAELKWKKDIRDEYWKVFQETTISTDKSFNE
ALKFHFASILLDELDAAGGLTKKQVTACLKPYIELLGNKDISEYLFTSLYEEIFKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: T00422 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="C47E12.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA93111.1"
/db_xref="PID:e1344635"
/db_xref="PID:g3875116"
/db_xref="GI:3875116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="predicted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="C47E12.7"
                                                                                                                                                                                                                                                                                                                 11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQENGDDVPDDEIAEVKKGNGKKTAVPKVKKGRPLLKAKGVGKKRMVGGLKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hetical protein YD78 (SW.YD78_YEAST); cDNA EST
T00422 comes from this gene; cDNA EST EMBL: C09139
from this gene; cDNA EST EMBL: C09139
cDNA EST, yk48266.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 comes from this
                                                                                                                                                                                                                                                                              Score 147;
Pred. No. 1.
0; Mismatc
                                                                                                                                                                                                                                                                                    Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .21126,21202.
.24224,24272 .
                                                                                                                                                                                                                                                                                                                                                                                                                                        Genefinder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITIRVSSLNPDFDNMVIVDDISYRATLCTDALSVF
AQDLSCDFSKRASACLWGMLNQDEESSEIASNSWTV
                                                                                                                                                                                                                                                                                                            DB 21;
.00e-92
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                                                                                                                                                                                                                                                                                                                                 Length 37855;
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                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .21506,21563.
.24411,25791. .
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Вb Ç В Çþ В

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140 ACATGGTGGTGGAGGTGCCACGTTGGACCAACGCGAAAATGGAGATTAGCTTGAAGACCC 199

Gaps

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ORIGIN
                                                                                    BASE COUNT
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AUTHORS
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ORGANISM
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LOCUS
DEFINITION
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      Matches
                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                 gene
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                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATAGCGAAGTTTTCCTTTTTTCACATCTTGTTTAATAGGGTTTAAAGGGTCCTTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAAGCGAGCTACACCCTTCTTCTCATCTTGCTTGATTGGCGAGAATGGTTCCTTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGTCTGAGGGATGGCACCATAGTTCCAGATATATCCTTTATACGGGAACAAATTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGTCTGTGGAAGAGCTCCGTAGTTCCAGATGTATCCTTTGTGTGGGGAAAATGTTGTGA 27494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAATTGGGTCATTGTCACCACAACAGCCAGTATGTTTATCATTGTGCCCTGGGTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAATTGGATCATTGTCTCCTTTAGCTCCAGTGTCAGGAACAACATGGTTTGGATCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
329; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inorganic pyrophosphatase is a component of the Drosophil nucleosome remodeling factor complex Genes Dev. 12 (20), 3206-3216 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gdula, D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Pterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila
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AF085601.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF085601 873 bp
Drosophila melanogaster
mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF08560:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 873)
pla,D.A., Sandaltzopoulos,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1
                                                                                   228
   Conservative
                                                                            NTIIAETHKFWONLVHOSPASGSISTTNITNRNSEHVIPKEEAEKILAEAPDGGQVEE
VSDTYDTWHFIHLK"
247 c 233 g 165 t
                                                                                                                                     /db_xref="G1:3600094"
/translation="malyetvekgaknspsyslyfknkcgnvispmhdiplyanbekt
iynmvvevprwtnakkeislktpmnpikodikkgklrevancfphkgyimnygalpot
wenpdhiedstgckgdndpidvieigyrvakkgdvlkvkvlgofalldegetdwkiia
                                                                                                                                                                                                                                                                                                                                                                                                                                                      37, Room 5E-20, Bethesda,
                                                                                                                                                                                                           /product="inorganic pyr
/protein_id="AAC97112.1
/db_xref="PID:g3600094"
                                                                                                                           IDVNDPLASKVNDIADVDQYFPGLLRATVEWFKIYKIPDGKPENQFAFNGDAKNADFA
                                                                                                                                                                                                                                                                        /note="nucleosome remodeling factor complex component"
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                 codon_start=1/
                                                                                                                                                                                                                                                                                                 /gene="Nurf-38"
                                                                                                                                                                                                                                                                                                                                /gene="Nurf-38"
                                                                                                                                                                                                                                                                                                                                                                               'Chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster
                  11.1%;
63.8%;
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Score 142; DB 22;
Pred. No. 1.44e-88;
0; Mismatches 187;
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                            Length 873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute,
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NURF-38 (Nurf-38)
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JOURNAL
MEDLINE
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                     The University, Dundee, DD 2 (bases 1 to 2887) Stark, M.J. and Milner, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-19: KLTRRIOC 2887 bp DNA PLN 10-FEB-19: Kluyveromyces lactis TRP1 gene, HHT1 gene and IPP gene for N·(5'-phosphoribosyl)anthranilate isomerase, histone H3 and inorganic pyrophosphatase (EC'3.6.1.1) respectively.
                                                                                                                                                                                                  Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a chromosomal locus flanked by genes encoding inorganic pyrophosphatase and histone H3 Yeast 5 (1), 35-50 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kluyveromyces lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHT1 gene; histone; histone H3; inorganic pyrophosphatase; IPP gene; isomerase; N-(5'-phosphoribosyl)anthranilate isomerase; '
                                                                                                                                                                                                                                                                                                                           Submitted (02-FEB-1989)
                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                   Stark, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Hemiascomycetes, Saccharomycetaceae, Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kluyveromyces lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; unidentified reading frame
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                                                                                                                                                                                                                                                                                                                                                                                    bases
                                                                                                                                                                                              (1), 35-50 (1989)
                                                      /organism="Kluyveromyces lactis"
/db_xref="taxon:28985"
/clone_lib="genomic in YCp50"
/clone="pJZB2, pJZB3"
24. 29
   /note≃"pot. TATA box"
                      /note=
78. .8
                                                                                                                                                           location/Qualifiers
                                     "pot. TATA box"
                                                                                                                                                                                                                                                                                                           Stark M.J.R.,
DD1 4HN, UK
                                                                                                                                                                                                                                                                                                                           Department of
                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales;
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142. .552
                                                                                                   /translation="MIKPNDFKKNTLCNCNCIQSDQIYTDPNVYPSTPTHEHRISHFL
NYRFFKHQSASFPSCRSLKUDDLRKKKLQNSYINRNEKCLHWFTIGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMVVEIPRWTNAKLEITKEEPLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWE
DPNESHPETKAVGDNDPLDVLEIGEQVAYTGQVKQVKVLGVMALLDEGETDWKVIAID
INDPLAPKLNDIEDVEKHLPGLLRATNEWFRIYKIPDGKPENQFAFSGEAKNKKYTLD
                                                                 /note="pot. TATA
                                                                                                                                                                                                                                                                                                                      complement (2486
                                                                                                                                                                                                                                                                                                                                                         complement(2475
                                                                                                                                                                                                                                                                                                                                                                                           complement(2453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="martKQTarkSTGGKAPRKQLASKAARKSAPSTGGVKKPHRYKP
GTVALREIRRFQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLV
                                                                                                                                                                                                                                                    complement(2524.
                                                                                                                                                                                                                                                                                      complement(2513
                                                                                                                                                                                                                                                                                                           /note="pot.
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="IPP open
                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /IRECNEAWKKLISGKSADAKKIDLTNTTLSDTATYSAEAASAVPAANVLPDEPIDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MSYTTRQVGAKNSLDYKVYIEKDGKPISAFHDIPLYADEANGIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:P13998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="inorganic pyrophosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="
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                                                                                                                                        'db_xref="SWISS-PROT:P13999"
                                                                                                                                                                             'db_xref="PID:g2904"
                                                                                                                                                                                            'protein_id="CAA32447.1"
                                                                                                                                                                                                                 codon_start-
                                                                                                                                                                                                                              'note="unidentified open
                                                                                                                                                                                                                                                                     'note="pot.
                                                                                                                                                                                                                                                                                                                                            'note="pot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .STAVHQQENVKGTKLVGVFRNQSVDDVLQLYHEYNLDVIQLHGDEDIKEYRSLIPSS
.PIIKRFQFPQDCELLLDLYEHVDNVLTLFDSGEGGTGEKLNWSAISSWSASHPEIKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="SWISS-PROT:P13997"
translation="MLVKVCGLQTVEAAKTAVDDGADYLGIICVPGRKRTIDSSVAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'protein_id="CAA32445.1"
'db_xref="PID:g2902"
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42. .745
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 10.8%;
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(2486. .2490)
TATA box"
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Length 2887;
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                                                                                                                                                                                                                                frame
                                                                                                                                                                                                                                (AA 1-91)
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63.6%;

No.:2.01e-84;

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGGCTCTTCCTTGGTAATTTCCAACTTGGCATTGGTCCAACGTGGAATTTCAACAACC .2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAACAAATTCGCAACATAGCGAAGTTTTCCTTTTTTCACATCTTGTTTAATAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCCTGGGTCTTCCCCAAGTCTGAGGGATGGCACCATAGTTCCAGATATATCCTTTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGTTTGGATCTTCCCATGTTTGTGGGAAGGCACCGTAGTTGTGAATGTAACCGTGATGT 2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGCCATAACACCAAGAACCTTGACTTGTTTCACTTGACCAGTGTAAGCAACTTGCTCA 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCATCAGGATCATCCACATTAATGGCAATGACTTTCCAGTCGGTTTCCCCTTCGTCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAGCTTCTAAGTAGCCAGGTTTCAGCCGTTTGACATCATTGATATCATTATAATTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGGCICTCAACAACCTGGTAAATGCTTTTCAACATCTTCGATGTCGTTCAACTTAGGA 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGCAAACTCATTTTCTGGTTTTCCAGCAGCAGCCTTATACCTTCTAAACCAGTCCACA 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTTGAAGATACCATTGGCTTCAT 2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGAAACAGTTTCTAACAAATCTTAACTTACCCTTCTTGGTGTCTTGAATAATTGGGTTC 2244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAATTTCACACACATCAATTGGGTCATTGTCACCACAACAGCCAGTATGTTTATCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGATTTCCAAGACATCCAATGGATCGTTGTCACCAACAGCCTTAGTCTCTGGGTGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGCCAATATGCCTAGAACTTTCACGCCAATTATTTCACCTCTTGCACATACCTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTGAAACACATCCTTATCTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGGGTCCTTTGTAGCAATCTCCATTTTTGCATTAGACCAGCGTGGTACTTCAACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS1042K10 184180 bp DNA PRI 21-JAN-1999
Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2.
Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2,
Adenylosuccinase, ASL) and 4 novel genes (one with probable rabgap domains and Src homology domain 3). Contains ESTs, STSS, GSSs and
                                                                                                           on Jan 22, 1999 this sequence version replaced gi:3927920. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission that the compared to the sequence submission.
                                                                                            corresponding to the overlapping clone, as we submit sequences
neighbouring
                                                                                 only a small
                                                                                                                                                                                                                              requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                     CB10 1SA,
                                                                                                                                                                                                                                                                     Submitted (23-DEC-1998) Sanger Centre, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                        It may be shorter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      putative CpG island,
AL022238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L022238.1 GI:4176442
                                                                                                                                                                                                                                                                                              rect Submission
                                                                                                                                                                                                                                                                                                                                   (bases 1 to 184180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenylosuccinate lyase; ADSL; ASL;
                   or longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                             UK. E-mail enquiries: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                           Catarrhini;
                                                                                                                                                                                                                                                                                                                                                Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Catarrhini; Hominidae; Homo.
                                                          This sequence is not
                                                                           overlap as described above
          sequence is not the entire insert of clone 1042K10. er because we only sequence overlapping sections because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CpG island;
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                                                                                                                                                                                                                                                                  Cambridgeshire
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rabGAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                 Clone
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repeat_region repeat_region

/note="MER46A repeat: 3999. .4074

.167

of consensus"

.82 of consensus"

matches

of.

consensus"

'note="Tigger4(Zombi) |581. .4879

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FEATURES
                     repeat_region
                                                                        repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1042K10 is from the library RPCI5 constructed at the Roswell Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr22
1042K10 is from the library RPCI5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping Group. Further information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was generated from part of bacterial clone contigs human chromosome 22, constructed by the Sanger Centre Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g. Alu). Where the sequence is ambiguous, using the 'unsure' feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence map criteria as follows. An attempt is made to resolve all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The true left end of clone 591N18 (AL031594) is at 184081 in sequence. The true right end of clone 377F16 (293783) is at in this sequence. This sequence has been finished according to
                                                                                                         GHNPTHLSNKMWKNHISSRNTTPLPRPPPGLTNPKPSSPWSSTAPRSVRGWGTQDSRLASASTWSDGGSVRPSYWLVLHNLTPQIDGSTLRTICMQHGPLLTFHLNLTQGTALIRY
                                                                                                                                                                                                       PKPHLDNMVPNALNVGLPDLQTKGPIPGYGSGFSSGGMDYGMVGGKEAGTESRFKQWT
SMMEGLPSVATQEANMHKNGAIVAPGKTRGGSPYNQFDIIPGDTLGGHTGPAGDSWLP
3826. .3970
/note="L1MB8
                                                                                             STKQEAAKAQTALH"
                                                                                                                                                              TDHQLLRDNTTGSNSSLNTSLPSPGAWPYSASDNSFTNVHSTSAKFPDYKSTWSPDPI
                                           note="MIR repeat: matches 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="supported by GENSCAN and FGENES; match: ESTs
AA615306 AA065323 W80019 N75651 AA747718 AA354286"
                                                                                                                                                                                                                                                  translation="RKISQAVRQQQEQQLARMVSALQQQQQQQQQQRQPGMKHSPSHPVG/
                                                                                                                                                                                                                                                                               'db_xref="GI:4176443"
                                                                                                                                                                                                                                                                                                   db_xref="PID:g4176443"
                                                                                                                                                                                                                                                                                                                           protein_id="CAA18263.1
db_xref="PID:e1371826"
                                                                                                                                                                                                                                                                                                                                                                        product="dJ1042K10
                                                                                                                                                                                                                                                                                                                                                                                            evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="dJ1042K10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786. .1903 note="FLAM_C repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="1042K10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="dJ1042K10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match: GSS B14103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSp repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluJb repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Alu repeat: matches 234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .n(<3190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :184180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .14879,15130.
.>23457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3233,3378. .3561,10740. .10877,13045. .9,15130. .15225,17511. .17735,18170. .:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches
                                                                                                                                                                                                                                                                                                                                                   (novel protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140.
                                             . 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .71 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .299 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .299 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .312 of consensus
                                        of consensus'
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                                   /note="match
27265. .2826
                                                                                                                                            /note-"match: ESTS A1006343 A1020127 A1011875 N59014
A1252767 A1011988 A1787828 AA699725 AA64865 AA631607
C87885 AA893853 AA782624 N64803 AA824572 AA927683 A17
A6632509 A1075774 AA811649 N58210 AA631607"
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                                                                   complement(26185.
                                                                /note="35 copies 2 mer gt
/note="35 copies 2 mer gt
/omnlement(26185. .26333)
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complement(20915 . .21365)
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/note="Charlie2 repeat: matches
                      note="match:
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21714 24027
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)494. 20787
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26. .19819
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                                                                                                                                                                                                                                                                                                                                                                                              e="AluY repeat:
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/note="match: ESTS Z42319 AI060394 W87941 W87940"

prim_transcript complement(33809. .3521)

/note="match: ESTS T04895 AI216324 AA935592 AA286708

AA809782 AA521409 AA400214 AA400125 T92466 AA573017

AA704714, AI248843 AA773853 AA136902 AA724710 AA629354
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/note="match: ESTs AA307016 AA375298 H73308 AA247913
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      204; Conse
                                                                            Submitted (14-OCT-1988) Kolakowski L.F., Univers. Pennsylvania, Department of Chemistry, 231 South Philadelphia, PA 19104
                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                               Saccharomyces cerevisiae
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                                                                                             IIKETHDSWKOLIAGKSSDSKGIDLTNVTLPDTPTYSKAASDAIPPASLKADAPIDKS
IDKWFFISGSV"
                                                                                                                                        /translation="mtyttrqjgakntleykvyjekdgkpvsafhdiplyadkennif
nmvveiprwinaklejtkeetlnpiiqdtkkgklëfvrncfphhgyihnygafpqtwe
dpnvshpetkavgdndpidvleigetlaytgqykqvkalgimalldegetdwkyjaid
                                                                                                                             INDPLAPKLNDIEDVEKYFPGLLRATNEWFRIYKIPDGKPENQFAFSGEAKNKKYALD
                                                                                                                                                                                                                                             /db_xref="SGD:L0000872"
/protein_id="CAA31629.1"
                                                                                                                                                                                                                                                                                /codon_start=1
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Score 131; DB 27;
Pred. No. 1.82e-79
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                                                    3 (bases 1 to 2411)
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8 (base)
Doignon, F., Domdey, H., Duesterhus, S., Dubois, E., Dujon, B
Bakkoury, M., Entian, K.D., Feuermann, M., Fiers, W., Fobo, G
Fritz, C., Gassenhuber, H., Glansdorff, N., Goffeau, A., Grij
                                                                                                                                                                                                                                                                                         Submitted (30-AUG-1994) Data collected by MIPS on behalf of the European yeast chromosome II sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                    Martinsried, FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baur,A., Boles,E., Miosga,T.,
Zimmermann,F.K.
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Z35880 Y13134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetaceae;
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                                                                                                                                                                                                                                                             E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li, Z.,
                                                        Demolis,N:, Delaveau,T.,
ubois,E., Dujon,B., El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermann, R.,
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                               Fobo, G.M.,
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                                                                                                                                                           Brandt, T.,
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                                                                                                                                                                                                                                                                                                                                                                                       718 AAATTCTGCATTAAACGCAAACTCATTTTCTGGTTTTCCATCAGGAACCTTATACCTTCT
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ACATACCTTGCTTCCAATTTCACACACATCAATTGGGTCATTGTCACCACAACAGCCAGT
                                             AGCAATAGTTTCACCAATTTCCAACACATCAATTGGATCGTTGTCACCAACTGCCTTAGT
                                                                                             CCCTTCGTCAATCATAGCCAATATGCCTAGAACTTTCACGCCAATTATTTCACCTCTTGC
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95112788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rad, M., Rieger, M., Rose, M., Schaaff-Gerstenschlaeger, I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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larity 61.8%;
Conservative
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/note="delta remnant"
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DPNVSHPETKA VGDNDPID VLEIGET I AYTGQVKQVKALGIMALLDEGETDWKVI AID
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/db_xref="PID:g536206"
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/db_xref="taxon:4932"
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translation="MTYTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 131; DB 27;
Pred. No. 1.82e-79;
0; Mismatches 213;
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E-28040 Madrid, SPAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-AUG-1997) Molina
II, Universidad Complutense de
E-28040 Madrid, SPAIN
Revised by [3]
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N-(5'.phosphoribosyl)anthranilate isomerase;
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Saccharomycetaceae; Pichia.
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                                                                                                                                                                                                                      /gene="TRP1"
350. .1063
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              /translation="MALVKICGLQSLEAAETAVNNGASLVGVIMVPGRERTVKQEVAR
EISQMVREKRISKGSKYLDSRQLRKEWDDCPLEDWFEYNVKEINSSGPFLVGVFRNQS
                                                 'db_xref="SWISS-PROT:013504"
                                                                                  'db_xref="PID:g2624378"
                                                                                                  'db_xref="PID:e1180017"
                                                                                                                                'product="N-(5'-phosphoribosyl)anthranilate isomerase"
                                                                                                                                                                                                  /gene="TRP1"
                                                                                                                                                                                                                                                                     'db_xref="taxon:4922"
                                                                                                                                                                                                                                                                                     /plasmid="pRS316-GAL1"
/strain="NRRL Y-11430"
                                                                                                                                                                                                                                                                                                                      organism="Pichia pastoris"
                                                                  'db_xref="GI:2624378"
                                                                                                                  protein_id="CAA04452
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Pichia pastoris TRP1, IPP1 and
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Nucleotide sequence of S. pombe inorganic pyrophosphatase
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Similarity 59.7%;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        746 GCAAGCCTGAAAATTCCTTTGCTTTCAGTGGTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          621 TGAAACCTGGCTACTTAGAAGCTACTGTGGACTGGTTTAGAAGGTATAAGGTTCCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 ATATGCCTGGCTTAATCCGTGCTAACGAGTGGTTCCGCATTTACAAGATCCCCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.pombe chromosome I
Z98559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-AUG-1995) Schizosaccharomyces pombe chromosome sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Car CB10 1RQ E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                     small overlap between neighbouring submissions. Cosmid c23C11 overlapped at the 3' end by c13F5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splice donor/acceptor sites. CDS are numbered using the following system eg SPAC5H10.01C. SP (s. pombe), A (Chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40s ribosomal protein; alanyl-trna synthetase; casein kinase i: ckal; dna mismatch repair; Homol D box; Homol E box; inorganic pyrophosphatase; mitochondrial dna repair; muts family; paired amphipathic helix; php3; plo1; polo box; ppa1; ribosomal prote:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in codons is given for each CDS IMPORTANT: This sequence MAY NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Details of yeast sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrell, B.G., Rajandream, M.A. and Wood, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s12; ribosomal protein s23; rps23; serine/threonine-protein kinase; transcriptional activator; zinc binding; zinc cadmium resistance protein; zinc metallopeptidases; zinc/cadmium resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the World Wide Web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brown, D. and Churcher, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fission yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 38391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/yeast/home.html)
join(217. 480,560. 874,928. 1113,1154. 1266,1352. 179
gene="SPAC23C11.01"
/note="SPAC23C11.01; len:441aa; similarity: eg. to
YILO90W, YIJO_YEAST, P40499, hypothetical 56.3 kd protein,
(491aa), fasta scores, opt:268,E():1.4e-19, (24.7%
                                                                                                                                                                                                                          /clone="cosmid c23C11"
                                                                                                                                                                                                                                                                                                                             organism="Schizosaccharomyces pombe"
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                                                                                                                                          'gene="SPAC23C11.01"
                                                                                                                                                                                                                                                     'chromosome="
                                                                                                                                                                                                                                                                           'db_xref="taxon:4896"
                                                                                                                                                                                                                                                                                                          'strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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cosmid c23C11.
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/note="SPAC23C11.03;
YJX2_YEAST, P47083, }
                                                                           /gene="$PAC23C11.03"
2923. .4719
                                                                                                                                                                                                                   complement (2633
                                                                                                                                                                                                                                                                                            complement(2366. .2389)
                                                                                                                                                                                                                                                                                                                                            /translåtion="mGKPAGLNAARKLRNHRREERWADAHYKKRLLGTAYKSSPFGGS
SHAKGIVVEKIGVEAKQPNSAIRKCVRVQLIKNGKKVTAFVPHDGCLNFVDENDEVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s23 homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ttaacattttttaacag, splice branch and acceptor"
complement(2103. 2583)
                                                                                                                      /note="Homol E box"
1923. 4710
                                                                                                                                                                                               /note="Homol D box"
                                                                                                                                                                                                                                                                                                                      SGFGRKGKAKGDIPGVRFKVVKVAGVGLSALFHEKKEKPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="
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SLEKPKFDYLPPNILQSVHYLISTISATLPRTLYNIVLFMVAAAKTVAPSVFATFAFI
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                                                  'gene="SPAC23C11.03"
                                                                                                                                                                                                                                               note="PS00055 Ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="40s ribosomal protein s23"
/protein_id="CAB11155.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SPAC23C11.01"
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                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="SWISS-PROT:P79057"
                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="GI:2330766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'protein_id="CAB11155.
'db_xref="PID:e334130'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="SPAC23C11.02c; len:143aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="PID:g2330766"
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                                                                                                                                                                                                                      .2640)
                         len:598aa, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splice branch and acceptor"
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                                                                                                                                                                                                                                               protein S12 signature"
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                    to YJR002W,
  593aa),
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overlap)"

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Note: remainder of
                                                                   Matches
                                                                                                                      Query Match
7422 ATGCTGAGAAGACCATCTTGAACATGGTCGTTGAGATCCCTCGTTGGACTCAGGCTAAGC 7481
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                                                                                              Similarity
                                                                   Conservative
                                                                                                                                                                 ,annotations omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="gtaagt, splice donor sequence"
complement(5354, .5377)
/gene="SPAC23C11.04c"
                                                                                                                                                                                                                                                                                                     pyrophosphatase
7198. .7203
                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5670.
                                                                                                                                                                                                                                                                                                                                        /note="EM_FUN:SPPPAG X54301 Yeast ppa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complemen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ctaaccaattctag, ;
complement(5039. .5044)
/gene="SPAC23C11.04c"
                                                                                                                                                                                                                                               note="putative TATA"
307. .8176
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RKMWIDIAQEFEIFIRCIHLQSSEELARHNNVFRYIHHNQKQLPEIAFNSFKSRFQMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRKPLTGMWNSFLKDVNRSIDLSFIKYVGDAAGRPGDHNSTDLKFAENI(
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                                                                                                                                                                                                                                                                                                                                                                           note="gtgagt, splice donor sequence"
157. .8475
                                                                                                                                                                                                                                                                                                                                                                                                                               gene="SPAC23C11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="ttaacatttttcaccctttag,complement(5670. .5675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="PS00017 ATP/GTP-binding site motif A (P-loop)" complement(5623. .5643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="SPAC23C11.04c"
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RPSNSLLDVDLEFETGAKPVPVQTEETTETLEDLIKNRIISKTFDDVPKRAPVAVTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="CAB11157.1"

'db_xref="PID:e334132"
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Complement(join(4842. .4988,5045.
/gene="SPAC23C11.04c"
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NDGFFDIDNFNKOTLALEEEAVEEGVLGDEDDGIDLLMDPDENMEDSEDESNGPQADS
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/protein_id="CAB11156.1"
/db_xref="PID:e334131"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="SPAC23C11.04c; len:42laa, similar eg. to C. elegans 1963, F21D5.5, (250aa), fasta scores, opt:395, ():1.1e-32, (41.7% identity in 223 aa-overlap)also imilar eg. to YMR156C, YM31_YEAST, Q03796, hypothetical 7.4 kd protein, (238aa), fasta scores, opt:156, ():4.8e-15, (32.5% identity in 206 aa overlap), contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPSELFELNENKSQRSLAEEYEEEFLKKSNADTYKSEADKKKEKEHEEIKALFSEVSR
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TRANSLATION="MTELINSEPTLFLEPNKEDSKOLVEKALEVESNIKIPSTSPIQTST
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                                                                                        59.7%;
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                                                        Score 100; DB 27; Length 38391;
Pred. No: 3.19e-54;
0; Mismatches 208; Indels 0;
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HPKNYLVRNSSSHPYHFKKSEHQEIVVLVGFPSSGKSTLAESQ
MYCYTYN
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VERSION
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                                                                                                                                                                                        Submitted (20-AUG-1998) LMCB, National Cancer Institute, NIH, Building 37 Room 5E-20, Bethesda, MD 20892-4255, USA
                                                                                                                                                                                                                                                                                Gdula, D.A., Sandaltzopoulos, R., Tsukiyama, T., Ossipow, V. and Inorganic pyrophosphatase is a component of the Drosophila nucleosome remodeling factor complex Genes Dev. 12 (20), 3206-3216 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF085600
                                                                                                                                                                                                                                  Gdula, D.A., Sandaltzopoulos, R., Tsukiyama, T.,
                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                            Drosophilidae; Drosophila
1 (bases 1 to 2826)
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda;
Pterygota; Diptera; Brachycera;
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2422. .258
                                        /géne="Nurf-38"
/product="NURF-38"
                                                                                                                   /chromosome="2"
                                                                                                                               /organism="Drosophila
/db_xref="taxon:7227"
                                                                                                                                                                              Location/Qualifiers
oin(642. .704,1148.
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NURF-38 (Nu
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Local Similarity 64.2%;
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                                                                                                                                                             1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                                                                                                                                                        Sequence 14
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/protein_id="AAC97111.1"
/db_xref="PID:93746880"
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1491 c 1486 g
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628 c 579
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ivnmvvevprwtnakmeislktpmnpikQdikkgklkfvancfphkgyiwnygalpQt
                                                                                                                                           Location/Qualifiers
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                 0.8%;
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Score 80; DB 25; Le Pred. No. 2.10e-38; 217; Mismatches 140;
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                                                                         IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Details of yeast sequencing at the Sanger Centre are available on the World Wide
                                                                                                                                                                                                                                   splice donor/acceptor sites. CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), 01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
Cosmid
                                                                                                                                                                                     in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                           Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct number of introns/exons or we may not have chosen the correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-MAY-1997) Schizosaccharomyces pombe chromosome sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Can
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Eukaryota; Fungi; Ascomycota; Archiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose-6-phosphate-1-dehydrogenase; inorganic pyrophosphatase; membrane transport; rna binding protein; rp118a-2; taf; tim complex subunit; transcription factor TFIID complex component; transcription initiation factor; tRNA-Cys; tRNA-Pro; y117b; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60s ribosomal protein; calmodulin; cam1; cysteine synthase; DNA-directed RNA polymerase II subunit; f0-f1 particle assembly;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1RQ E-mail:
http://www.sanger.ac.uk/Projects/S_pombe/)
d c3A12 overlapped by c20G8 at the 5'end.
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     /gene="SPAC3A12:02"
                                                                                /gene="SPAC3A12:02"
                                                                                                                                                                                                                                                                                              /note="Pfam match to entry pr00719
                                                                                                                                                                                                                                                                                                                                                                                                        EPYFHTIPNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MASLAKNILQFRSKITGKLNTPDFRVYCYKNNKPISFFHDVPLT
SDKDTFNMYTEIPRWTQAKCEISLTSPFHPIKQDLKNGKLRYVANSFPYHGFIWNYGA
LPQTWEDDNVIDSRTKMKGD6DPLDVCEIGG8IGYIGQIKQVKVLGALGLIDQGETDW
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                                                      note="PS00387 Inorganic"
                                                                                                                                                                                                                                                                                                                                                       /gene="SPAC3A12:02"
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                                                                                                                                                   'note="ctaacaattttttcaactag,
                                                                                                                                                                                  'gene="SPAC3A12.02"
                                                                                                                                                                                                                                                        'gene="SPAC3A12;02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product="inorganic pyrophosphatase"
'protein_id="CAB08747.1"
'db_xref="PID:e316097"
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|oin(2563...2718,7827...3199,3258...3589)
|gene="SpAc3A12.02".
|ote="SpAc3A12.02". len:286aa, similar eg. to IPYR_SCHPO,
|19117, inorganic pyrophosphatase, (288 aa), fasta scores,
|pt: 930, E():0, (48.7% identity in 277 aa overlap), also
|pt: 930, E():0, (48.7% identity in 277 aa overlap), also
|similar eg. to YERQIIC, IPYR_YEAST_PO0817, inorganic
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/db_xref="GI:2462674"
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/protein_id="CAB08758.1"
/protein_id="CAB08758.1"
/db_xref="pib:e351362"
/db_xref="pib:e351362"
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/note="SPAC3A12.01c,
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GESDDQMNSSSEDYPAQRLQLYKKTISEGDYNFDNVPPPELRTPTLDSFVVLPAAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="SWISS-PROT:P87117"
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/gene="SPAC3A12.01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rophosphatase, (286 aa), fasta s
4.4% identity in 250 aa overlap)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )_xref="PID:g2104418"
)_xref="GI:2104418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _xref="SWISS-PROT:P87118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEKNSPEEVNDLFSWKIEIYNRIFDLLSSKTKVDHPLCVECAELLTEEMSKTLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "SPAC3A12.01c, similarity: to YPL120W, (557aa), fasta scores, opt:391, E():4 ty in 344 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tRNA-Cys, anticodon gca, length = 73"
                                                                                                                                                                                                                           splice.
                                                                                                                                                                                                                           donor sequence"
                                                   pyrophosphatase signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fasta scores, opt:
                                                                                                                                                   splice branch and acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pombe"
                                                                                                                                                                                                                                                                                                                        Pyrophosphatase,
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                                                                                                                                                                                                                                                          /note="ctaacttag, splice branch and acceptor sequence" complement(6013 .6018)
/gene="SPAC3A12.04c"
                                                                                                               complement(join(6860. .7795,7836. .10215,10291. .10301))
/gene="SPAC3A12.05c"
/note="SPAC3A12.05c, putative transcription initiation
                                                                                                                                                                                       /note="gtatgg, splice donor sequence" complement(6860. .10301)
/gene="SPAC3A12.05c"
                    fasta scores, opt:1598, E():0, (31.0% identity in 1226 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                    /note="gtacgt, splice donor complement(5977. .5985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5809. .5823)
/gene="SPAC3A12.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYSRITLTIESMPQNKVLSNVTKEFDILAIRPIGDRLLQQTCSDLEFDILSIDFTQRL
PFYLKHTFMGLAVSRDIGIEISYSSGLRDVSNRRNLIINATSLVRATRGRGIIVTSET
RTPLECRAGFDVINLATFWDLKQDQARKSVGESCRSVLLHAETRRDTYRSILNGCH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SPAC3A12.04c, len:216aa, similar eg. to YHR062C, YHM2_YEAST, P38786, hypothetical 32.2 kd protein, (293aa), fasta scores, opt:420, E():4e-22, (34.9% identity in 218 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SPAC3A12.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDSRTHSAETDRSLLSAMSVRNSRMPYIVSSTL"
                                                                                                                                                                                                                                                                                                                                             /gene="SPAC3A12.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(5344. .5808,5878.
/gene="SPAC3A12.04c"
/note="SPAC3A12.04c, len:216aa, si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match
C3HC4 type"
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3245 ..3257
/gene="SPAC3A12.02"
codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also similar to GOLI_DROME, Q06003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   090972, RING ZINC FINGER PROTEIN, (381 aa opt:214, E():1.4e-07, (37.3% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3887 . .4816)
/gene="SPAC3A12.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="SPAC3A12.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="ctaacattgccttag,
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'translation="MINFTYLQKVGYTAIALNYQYDGKLQNVIKNPIVKELYPEQKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical
/protein_id="CAB08749.1"
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/translation="MPIPKNRPMHYEEEVSSQTNTEILLFALVIILSVIFINFFFFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein), (284 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3887. .48
/gene="SPAC3A12.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'protein_id="CAB08749.
'db_xref="PID:e316098"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Zinc finger, C3HC4 type"
/protein_id="CAB08748.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (36.5% identity in 74 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="PID:g2104420"
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                                                                     transcription
                                                                                          len:1108aa,
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                                                                                     , putative transcription similar eg. to YCR42C, 7
                                                                     initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splice branch and acceptor sequence"
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goliath protein (gl
pt:203, E():6e-07,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3072 AATCGGCTACATTGGGCAAATCAAGCAAGTAAAAGTTCTCGGTGCATTGGGTCTTATCGA 3131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2892 CATCAAGCAGGATCTAAAAAAATGGAAAGCTGCGTTATGTTGCCAATTCCTTTCCTTACCA 2951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens full length AF086012
mailto:est@watson.wustl.edu
                                                    Genome Sequencing Center
Department of Genetics
Washington University
                                                                                                                            Direct Submission
Submitted (24-AUG-1998) Departmen
University, 4444 Forest Park Aven
                                                                                                                                                                                                                                                                                                                                      marth,G., Bowles,L.; Wylie,T.,
Geisel,S., Allen,M., Underwood
                                                                                                                SUBMITTED BY:
                                                                                                                                                                                                                                                              Full Clone Sequencing
                                                                                                                                                                                                                                                                                    Wilson, R. and Waterston, R
                                                                                                                                                                                                                                                                                                      Schurk, R., Ritter, E., Kohn, S., Swaller, T.,
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                                                                                                                                                                                                                                                                                                                                                                                  Woessner, J., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Cl
Primates; Catarrhini;
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                                                                                                                                                                                                                                                Unigene Cluster
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                Louis MO 63108, USA
p://genome.wustl.edu/gsc
                                                                                                                                                                                                          (bases 1 to 460)
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component"
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/db_xref="PID:e316099"
/db_xref="PID:92104421"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Vertebrata; Mammalia; Eutheria;
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                                                                                                                                Avenue,
                                                                                                                                                                                                                                                                                                                        Chamberlain, A., Morales, R
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                f Genetics, Washington St. Louis, Missouri 63108, USA
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NOTICE:

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                                                                                                                                                                                  264 AGATTGCTACAAAGGACCCTTTAAACCCTATTAAACAAGATGTGAAAAAAAGGAAAACTTC 323
AG
                                                                                                                                                                                                          AGATTGCCACCAAGGAGCCAATGAATCCCATTAAACAATATGTAAAGGATGGAAAGCTAC 208
                                                                                        GCTATGTTGCGAATTTGTTCCCGTATAAAGGATATATCTGGAACTATGGTGCCATCCCTC 383
                            _ 8
                                                                                                                                       SIMILARITY INFORMATION: similar to Bos taurus protein P37980 (PID:g585322) INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The location of this clone is unknown Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly consensus quality values for this sequence have been submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved.

Nevertheless, we are confident of the accuracy of this sequence as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attempt has been made to verify whether this continued the original mRNA from which the full-length of the original mRNA from which it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         separately.
                                                                                                                                                                                                                                                                             h 5.5%;
Similarity 78.7%;
96; Conservative
385
                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                                  (PID:g124873)
67 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PID:g124871)"
151. .270
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to Caenorhabditis elegans
(PID:91167477)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Morton_Fetal_Cochlea"
/clone="IMAGE:252618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar to Kluyveromyces lactis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PID: 93219813)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to Schizosaccharomyces pombe protein P87118/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to Bos taurus protein P37980 (PID:g585322)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            made to verify whether this corresponds to the he original mRNA from which it was derived. We
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Pred. No. 1.05e-30;
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                                                                                                                       Score
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Oligonucleotide probe Base substituted E.co
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ALIGNMENTS

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SCCCCCPPT PD PRPPT
Query Match 100.0%;
Best Local Similarity 100.0%;
                                               and tissue I
                                                                       The present sequence encodes a human inorganic pyrophosphatase designated HPYP. Nucleic acids encoding HPYP were first identified in Incyte clone 768320 from the lung tissue cDNA library LUNGNOTO4. The recombinant pyrophosphatase, may be useful in promoting cell
                                                                                                                                                                                                                                                                                                                                                   Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                  cell
                                                                                                                                                                 DNA encoding human pyrophosphatase protein - useful for producing recombinant protein, which may be useful in promoting cell and
                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC:
Hawkins PR, Hillman JL;
WPI; 99-044570/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          V63542 standard; cDNA; 1275
V63542;
                                                                                                                                   Claim 3; Fig 3A-D;
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n; tissuė regenera
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Score 1274; DB 54; Pred. No. 0.00e+00;
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:lone 768320;
            Length 1275;
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DNA sequence

Matches

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                                                                                                                                                                                                                                                                                                                    30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
         New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders Claim 1; Page 233-234; 385p; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. X00602) for increasing the stability of the fused protein as
                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia, developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X00685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
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99-070066/06.
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US-048350.

US-048351.

US-048352.

US-048355.

US-054804.
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JS, Lafleur DV
n SM, Shi Y, Y
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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aagtgtgatcctgatgctgccagagccattgtggatgctttaccaccaccctgtgaatct
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larity 99.6%;
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
05-AUG-1997;
                                                                                                                                                                                                                                                                                                                              Human secreted protein gene 75 clone HOSE145.
Human secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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W09842738-A1.
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X00716 standard; DNA; 1350
X00716;
25-MAR-1999 (first entry)
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) HUMAN GENOME
LA, Duan R, Eb
JM, Hu JS, Laf
                                                   US-041277.
US-041277.
US-041281.
US-042344.
US-048094.
US-048095.
US-048095.
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T21836;
T21836;
01-AUG-1996
               Claim 1; Page 977; 2245pp; Japanese.

Claim 1; Page 977; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared sequences were obtained from 3'-directed CDNA as initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from various human tissues; so of cDNA was initiated from the from the from the first the f
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mRNA by using poly(T)
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Matches, 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     untranslated sequence is unique to a particular mRNA species, almos all the 3'-oriented cDNAs hybridise with specific mRNAs. Each libra is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. Sequence 416 BP; 128 A; 77 C; 77 G; 128 T;
                                             Oligonucleotide probe MK14-A consists of (QS1735). It hybridized to all sp. of m cross reacted to a few non-mycobacterial be useful as an initial screen for mycobase also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15
                                                                                                                              WPI; 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria -
detection and amplification of Mycobacteria nucleic acid
                                                                                                                                                                              (BECT ) BECTON DICKINSON Shank DD, Spears PA;
                                                                                                                                                                                                                                                                             Oligonucleotide probe Oligonucleotide; DNA p
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                                                                                                                                                                                                                                         Synthetic.
EP-571911-A.
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Claim 3; Page 14;
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24-MAY-1993; 108325.
26-MAY-1992; US-889651
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Pred.
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                       Score 44;
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1. No. 2.18e-247;
1. he-thes 8;
  Mismatches
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                                                                              s of nucleotides 5-95 of of mycobacteria tested, rial spp. The probe may
            2.95e-11;
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                                                                                                                                                                                                                                                                               disease
5
                       Length 91;
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24-MAY-1993; US-889651.
26-MAY-1992; US-889651.
(BECT) BECTON DICKINSON C
Shank DD, Spears PA;
WPI; 93-3788447...
New oligo:nucleotide probes
Netection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                 Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are completed to forms that can amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of wh
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Introducing random point mut
by prepn of single stranded
by prepn of single stranded
                                                                                                                            Oligonucleotide;
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31-MAY-1994
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Lehtovaara P,
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03-APR-1987;
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08-NOV-1990
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N81164
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11; Conse
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                                                                                                                                                                                                                                                                                                                                                                   204
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US-034819.
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                                                                                                                                                   entry)
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                                                                                                                             probe;
                                                                                                                                         MK14-A
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                                                                                                                                                                           BP
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Pred. No.
       specific for Mycobacteria of Mycobacteria nucleic a
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                                                                                                                                                                                                                                                                                                                    Pred.
53; 1
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                 used
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Best Local
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Best Local
                     Q70465 standard; DNA; 114 Q70465;
                                                                                                                                                                                                                                                                  single stranded template and an oligonuclectide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
05-APR-1995
                                                                                                             153
                                                                                                                                     995
                                                                                                                                                                                                                                      occurred singularly in any See also P80575. Sequence 204 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                            Random point mutations were introduced into the alpha E.coli beta-galactosidase. The wild type sequence was
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 by prepn of single stranded template, annealing a primer misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                             Introducing random point mutations int by prepn of single stranded template,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J,
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cross reacted to a few non-mycobacterial be useful as an initial screen for mycoba see also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15
                                                                                    935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-1990
                                                                                                                                                  93 hyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncn 152
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                                                                                                                            ATGTAGCAATATCAGCTTGTATTCCAGAGAAATCTCATTAGTTTTTCTGGTGATGGAACC 936
                                                                               ACTTATCCACGTCTGTTGGTACTGTGCAGG
                                                                                                       cccbnnhvchnvhbnnhrnwayvrhdarrd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OV-1990 (first entry) substituted E coli beta-galactosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta
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                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
     (first entry)
                                                                                                                                                                                   3.1%;
larity 6.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            galactosidase alpha-fragment;
coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                               ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВÞ
                                                                                                                                                                                                                                                             given mutant.
                                                                                                                                                                                   Score 40;
Pred. No.
52; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                      47
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                                                                               906
                                                                                                       182
                                                                                                                                                                                                                                   17 G;
                                                                                                                                                                                            DB 1; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; I
5.93e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic
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obtained
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Best Local S
Matches
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                                                                                                          Generic DNA sequence to generate a random TSAR; totally synthetic affinity reagent; effector domain; concateneated heterofunct
misc_feature
                                                     Synthetic.
                                                                                                                                                                                                                                        070468 standard;
070468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compans. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion,
                                                                                                                                                                                                            05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Y are flanking restriction sites (X is not the same as Y) that are not specified further: Other generic sequences are shown in 070466-68. Other specific peptides generated by these generic sequences are shown in 65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions—a binding domain with affinity for a ligand and a second effector peptide portion that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have design activity allowing direct and rapid detection in a screening procedure of the production of the product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        radioisotope, peptide, toxin or enzyme, to the specific target or on cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the neem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English. Q70465 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNC-) UNIV NORTH FOWLKES DM, Kay BK WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9418318-A
18-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                            91 GAGCGGCTTCAGCACCGAGGAGCGCGCGCCCCTTCTCCCCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 5; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCGCGCGTGCGGGTGGTGGCTCTGTGGCAGCGGCGGCGGCAGGACTCCGGCACTAT
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                                                                                    rapid;
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                                                                                                                                                                                                   (first entry)
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                                                                                    detection;
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Location/Qualifiers 55..60
                                                                              concateneated heterotection; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //*tag= a
/note= "this sequence r
sequence of 6, 9 or 12
comments)"
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                                                                                                                                                                                                                                                              ВP
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Pred.
32; M
                                                                                                       heterofunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No. 1.04e-06;
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                                                                                                                                       TSAR petide
synthetic; k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                           generic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and have designed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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PS Disclosure; Page 35; 255pp; English.

C Q70468 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be CC represented as follows: X(NNB)11(TGC)(NNB)5Z(NNB)7(TGC)(NNB)10Y. X CC and Y are flanking restriction sites (X is not the same as Y) that are CC enot specific peptides generated by these generic sequences are shown in Q70466-68.

CC Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, CC comprising at least two functional regions - a binding domain with CC affinity for a ligand and a second effector peptide portion that is CC chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues
                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                            Metzger
WPI; 97-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.
              Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                  06-JUN-1996; U09306.
07-JUN-1995; US-4744
                                                                                                                                                                                                          Human RANTES antisense oligonucleotide.
Asthma; airway epithelium; adenosine free;
Chronic obstructive pulmonary disease; bron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNC-) UNIV NORTH Fowlkes DM, Kay B
                                                                                                                                                                                                                                                                                              T 11
T76307 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R65154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1993; US-176500.
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                                                                                                                                                          19-DEC-
                                                                                                                                                                                                                                                                        5-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 TCGGTACTCCAGGGAGAAGGGCGCGCGCGCTCCTCGGTGCTGAAGCCGCTCATAGTGCC 83
                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                    63 bnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 bnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnnnnnnnn 62
                                                          97-051871/05
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                                                                                              UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                US-474497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay BK;
                                                                          Nyce JW;
                                                                                                                                                                                                                                                                    (first entry
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                                                                                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%;
                                                                                                                                                                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36;
Pred. No.
33; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents 'Z'; Z
6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.04e-06;
                                                                                                                                                                                                              ree; cystic fibrosis; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 114;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subject. The present sequence is an antisense oligonuclectide specific for the human RANYES, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating
                                                                                                                                                        Administration of the consensus sequence of an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene there were the conservative replication of pure conservative vectors for gene conservative replication of pure conservative vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYMC-) UNIV McGILL.

Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos
WPI; 98-362770/31.
                                                         therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned human telomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 162 BP; 0 A; 29 C; 74 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenosine from the antisense ON, its liberation upon antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A method
                                                                                                                                                                                                                                                                                                                      This sequence represents a human or mammalian DNA replication or consensus sequences of the invention, designated uniorsconsensus
                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 42; 54pp; English. This sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                     inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human or mammalian origin of replication consensus sequences -
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21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
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  Sequence
                                        linear,
                                                                                                                                                                                                                                                                                                                                                                                      artificial
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Similarity 42.9%;
54; Conservative
                                      large or small yeast artificial chromosomes (YACs) or as episomal
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  91
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  B₽;
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15; A;
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Pred. No. 1.04e
29; Mismatches
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1.04e-06;
---hes 42;
4 G;
  7 T;
                                                                                                                                                                                                                                                                                                                                            DNA replication origin
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Query Match

Score 34;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; page 35; 255pp; English.

O70469 is a generic DNA sequence used to generate random TSAR peptid This generic formula can be represented as follows: X(TGC)(NNB)10-(TGC)(NNB)2(TGC)(NNB)14(TGC)X and Y are flanking restrict sites (X is not the same as Y) that are not specified further. This sequence generates peptides that are cloverleaf in structure. Other
                                                                                                                                                                                  formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                        generic sequences are shown in Q70465-68. Other specific peptides generated by these generic sequences are shown in R65150-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, oriflanking the
                                                                                                                                                                         detection
                                                                                                                                                                                                                                                                             or enzyme,
                                                                                                                                                                                                                                                          biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace
                                                                                                                                                                                                                                                                                                     unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNC-) UNIV NORTH CAROLINA FOwlkes DM, Kay BK; WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
                                                                                                                                                                                                                                            the function of macromolecules, eg. monoclonal or polyclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 effector domain;
direct; rapid; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Л 13
Q70469 standard; DNA; 114 ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 TGAAATTGGAAGCAAGGTATGTGCAAGAGGTGAAATAATTGGCGTGAAAGTTCTAGGCAT 516
31 CGGCGCCGCGTGCGGGTGGTGGCTCTGTGGCAGCGCGGCGGCGCAGGACTCCGGCACTAT
                                67 wkawsdatakwwwkda
                                                                                                                                                                                                        therefore circumvent the need for complex methods of hybridoma mation or in vivo antibody production. The TSARs, are easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 krawrwwkkdav-wwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrkmwwt 66
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                                                                            Similarity 4.7% 5; Conservative
                                                                                                                                                       in a screening
114 BP; 0 A
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "this sequence represents 'Z';
sequence of 6,9 or 12 nucleotides (see
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                                                                                           2.7%;
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                                                                                                                                                                   process
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Pred.
32; M
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No.
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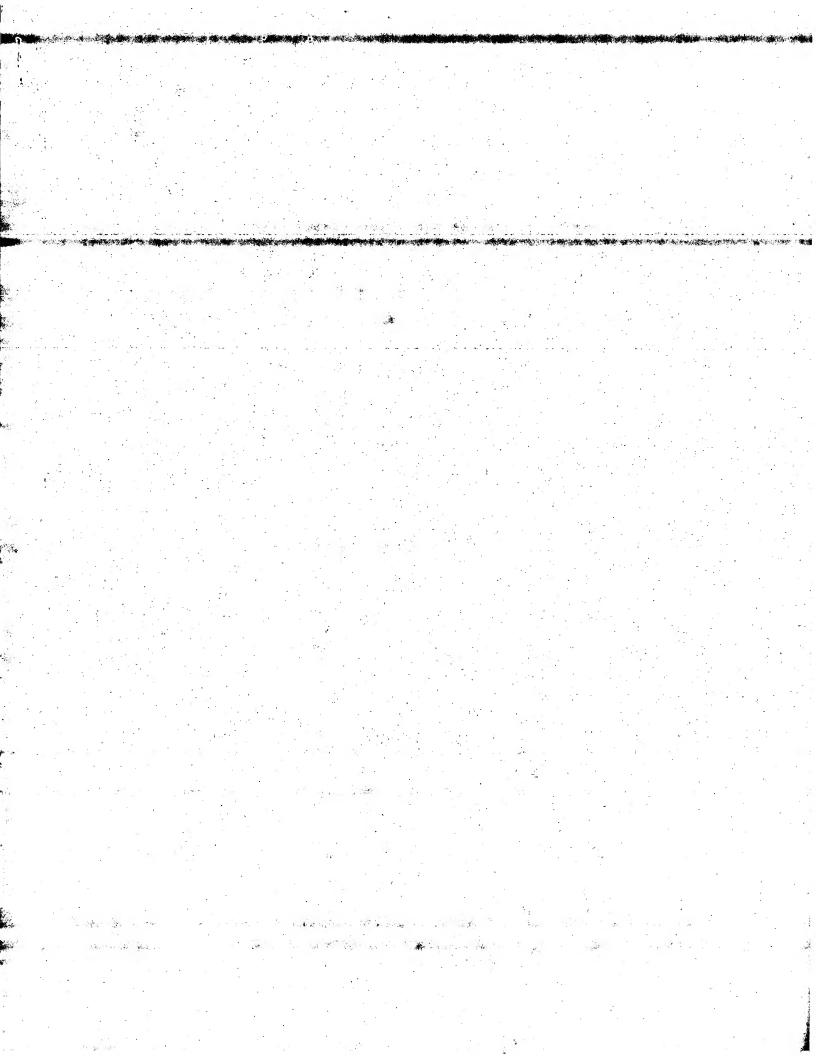
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Fowlkes DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65153.
Identifying proteins or peptide(s) which bind a ligand - by
Screening a recombinant vector library expressing fusion proteins
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		PYROPHOSPHATAS		Sequence 27, Appli Sequence 1, Appli Sequence 145, Appli Sequence 143, Appli Sequence 142, Appli Sequence 142, Appli Sequence 142, Appli Sequence 92, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 95, Appli Sequence 95, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 10, Appli	

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JENCE 1275 BP;
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                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                          TELEPHONE:
                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                   REGISTRATION NUMBER: . 29,768
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                 LENGTH:
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: 7218 base pairs nucleic acid EDNESS: single
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(703)683-4109 (703)836-9300

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EP 91 114 300.6

US/07/935,313

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Sequence 14, Application Sequence 14, Application
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                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                 APPLICATION NUMBER:
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
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                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0
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CLONE: pTZgpt-
                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
           TELECOMMUNICATION INFORMATION:
                                               ATTORNEY/AGENT INFORMATION: NAME: Hanson, No. 579596
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                    APPLICATION NUMBER: FILING DATE: 14-FE CLASSIFICATION:
                                 NAME: Hanson, No. 5795961man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                            STREET:
                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                               Kunio
                                                                                                                  Release #1.0, Version #1.30
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Pred. No.
                       LUD 5409
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                  TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         885 MTSSSSASVGDRVTTCRSSTTHGNGNTYYWYKGKAKYRVSNRSGVSRSGSGSGTDY 940
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Local Similarity 12.9%;
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                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                      FEATURE
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TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
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                                                                                  MOLECULE TYPE:
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           LOCATION: 1.215
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                       REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                   NAME: , Bastian, Kevin L
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sequence
8 C; 25 G;
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US/08238163
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                           /standard_name= "Deduced amino acid
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Pred. No.
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of PGIP
26 T; 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-388-672A-22 STANDARD; DNA; UNC; 965
                                                                                                                        SEQUENCE 965
780 KGURHUVHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYINYNGKRGRVIMADTS 839
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Local Similarity 13.3%;
hes 20; Conservat;
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                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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Similarity 13.6%;
25; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Human Anti-Lewis B Antibodies
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                                                             Score 28; DB 3; 1
Pred. No. 4.80e-04
83; Mismatches 7
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Pred. No. 4.80e-04;
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                                                                                                                        226 G;
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Best Local :
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                                                                SEQUENCE 215 BP;
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                                                                                                                                                                                                                                                 TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
              Match 2.1%;
Local Similarity 15.0%;
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
                                                                                                                                 PEATURE:
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                                                                              OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                LOCATION:
                                                                                                                                                                                      TOPOLOGY:
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LABAVITCH, John M
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                                                                                                                                 misc_feature
                                                                                                                                                                                      unknown
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                                                             MATION: /standard_name= "Deduced amino MATION: sequence of PGIP from bean." 15 A; 8 C; 25 G; 26 T; 141 OTHER.
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Score 27; DB 1; Let
Pred. No. 1.85e-03;
65; Mismatches 75;
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Best Local Similarity
Matches 6; Conser
                 Sequence 143, Application US/08471052A Sequence 143, Application US/08471052A Patent No. 5625033
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: SEQUENCE 65 BP; 3
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                                                                                 XXXXXX
                                                                                           US-08-471-052A-143 STANDARD; DNA; UNC; 68
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Sequence 145,
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    GENERAL INFORMATION:
                                                                                                                                                             384
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin NoTa:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
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NAME: Misrock, S. Leslie
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                                                                                                                                                       AGACTTGGGAAGACCCAGGGCACAATGATAAACATACTGGCTGTTGTGGTGACAATGACC 443
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                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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Application US/08471052A
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A; 3 C; 3 G; 2 T; 54 OTHER.
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                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LENGTH: 68 bases
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                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
                             APPLICATION NUMBER:
                                                                                                                                                       COUNTRY:
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REFERENCE/DOCKET NUMBER:
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1155 Avenue of the Americas
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1155 Avenue of the Americas
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SYSTEM: PC-DOS/MS-DOS
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                             PCT/US95/11934
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Best Local Similarity

Matches 6; Conse
                                                        TELEX: 66.41 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base --
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Antigen Binding Peptides (Abtides).
NUMBER OF SEQUENCES: 103
CORRESPONDENCES: 103
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MEDIUM TYPE: Floppy disk
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MOLECULE TYPE:
UENCE 75 BP; 1
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                                         STRANDEDNESS:
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(212) 869-9741/8864
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Pred. No. 9:22e-02
20; Mismatches 4
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Best Local Similarity
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                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER
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                                                      442 GTCATTGTCACCACAACAGCCAGTATGTTTATCATTGTGCCCCTGGGTCTTCCCCAAGTCTG 383
382 AGGGATG 376
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                                                                                 Local Similarity
                          65 NBGGTTG 71
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LENGTH: 75 base pairs
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cytogen TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fennie & Lancing STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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PC/TUS9511934
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Pred. No. 9.22e-02;
20; Mismatches 40
                                                                                                            Score 24; DB 4;
Pred. No. 9.22e-02
20; Mismatches 4
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RESULT 12 ID PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
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                                                                              NUMBER OF SEQUENCES: 1
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                                                                                                                                       APPLICANT:
                                                                                                      PPLICANT: Cytogen Corporation ITLE OF INVENTION: Antigen Bir ITLE OF INVENTION: Peptide Lii
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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              COUNTRY:
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10036
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                                                                                            Antigen Binding Peptides (Abtides) From Peptide Libraries : 103
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Pred. No.
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Best Local Similarity
Matches 5; Conse
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 20-SEP-19
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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Pred. No. 9.22e-
20; Mismatches
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                                  1101-196-228
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9.22e-02
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS

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Matches
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Sequence 94, Application PC/TUS9511934
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72 NBGGTTG 78
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                                                                                                                                                              INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
'STRANDEDNESS: Single
TOPDIOGY 1:000
                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                            TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,8 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 20-SEP-1995
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                                                                                                                                                                                                                                                              66141 PENNIE
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1155 Avenue of the Americas
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                                                    Score 23;
Pred. No.
20; Misma
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                                                       Mismatches
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                                                                        3.24e-01;
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